

Appendix

Appendix Table S1. Chi-square test for segregation ration of normal and mutant plants in the F₂ generation (*Gmlmm1-1* × Hedou 12)..... (Page 1)

Appendix Table S2. INDEL molecular markers for fine-mapping.....(Page 1)

Appendix Table S3. Thirteen genes in the mapping region.....(Page 2)

Appendix Table S4. Homology analysis of malectin-like RK family members on Chromosome 13 in soybean.....(Page 3)

Appendix Table S5. Comparison of plant height, main stem node number and other yield traits.....(Page 3)

Appendix Table S6. Chi-square test for segregation ration of F₂ generation (*Gmlmm1-1* × *Gmlmm1-2*).....(Page 3)

Appendix Table S7. Primers used in this study.....(Page 4)

Appendix Table S1. Chi-square test for segregation ration of normal and mutant plants in the F2 generation (*Gmlmm1-1* × Hedou 12)

Cross	Generation	No. of plants/lines		Mutant type	Expected ratio	χ^2	<i>p</i>	<i>df</i>
		Total	Wild type					
<i>Gmlmm1-1</i> × Hedou 12	F2	464	372	92	3:1	3.28	0.07021	1

Appendix Table S2. INDEL molecular markers for fine-mapping

Primers	Chromosome	Physical position	Sequence 5'→3'
MOL3644&MOL3645	Gm13	9591880	TTAGCCCTGTTTACCTCAATCC GACCCCTTCCTTTGACTGTTGC
MOL3646&MOL3647	Gm13	10007800	ACGGAAGAAAGATTGTTTCATGG CGATGTAGGGGCAAAATGG
MOL3650&MOL3651	Gm13	13891579	AGGCTCACCTCCGCAGATAG CGGCACAGACTGAGCAATAGAG
MOL3652&MOL3653	Gm13	14046684	AGAAAGCCTATGTCGGCAAGA TCAAAGGGTGCTCCTCACA
MOL3654&MOL3655	Gm13	15477038	CATCCACCATGAAAATTAACCC CAATCATCAAAATCCCATCCCT
MOL3678&MOL3679	Gm13	14537849	CCAAGGGACTGTGAGGTGAAC GGATGGACAACCTCAAGAAGAA
MOL3680&MOL3681	Gm13	14653018	ATGCACTCGTTTGACAAATTC GCTTCTGCATTGACATGACGC
MOL3682&MOL3683	Gm13	14778920	TGCGAGATCCAATGTGGTTAC TGTAGGTTGCGTCTCGTTTGT
MOL3684&MOL3685	Gm13	15061138	TACATGGAGCGTGCTTATCAAA TGTTGACCAATATGCGTGTCTT
MOL3686&MOL3687	Gm13	15508918	GGGAGATTTCACATCAAGTTCG TGAGGATGGGAAACCAGTCAGT
MOL3688&MOL3689	Gm13	16048790	TCCCTGTTTGGCTTCAGTCTAC CGGAGCTGTTGCACCTTTGT
MOL3692&MOL3693	Gm13	16787574	TGGTCGCATGACATCATAACAA CATTGGCTGGAATGAGAAGC
MOL3754&MOL3755	Gm13	15077108	CAAGAAGCACCCACCCA CGATGAAGACGGTGACAGTGAG
MOL3756&MOL3757	Gm13	15131757	GTCGTGGTTTCGCAAGAAAGC TGGCCTCGTTGAGCAAATC
MOL3758&MOL3759	Gm13	15231494	CCAAAAGGAGCAGAAAGTCAAG TTGAGTGAAGCCAAGGAGGAG
MOL3760&MOL3761	Gm13	15233406	CTCAATCTCCCTTACCCCTTTT

MOL3770&MOL3771	Gm13	15133035	GTGGGAACTCGTTCTGTATCGT AAGGAGCGGTATGAGGGAGC CAATGCCACTGCACAAGAAAC
MOL3772&MOL3773	Gm13	15158889	TTCTAAAACCTCCACCCC CAGTTGGGTGTATTGAAGGCT
MOL3774&MOL3775	Gm13	15160087	GCCTGATAGATGCGACAAAGTT GACCTTAAATGCACGTCGTTG
MOL3776&MOL3777	Gm13	15221786	TGGATTGCTTAGTTCCAAGACG CCAAATCGTTGCCAATAAGG
MOL3778&MOL3779	Gm13	15188188	GCCACTGCTTTTGAAGTGGATG AATGCCAAAGGTGAATCGTG
MOL3780&MOL3781	Gm13	15208153	TTTCCCTTAAAAGGTAAATCC GGTCAATAGTCAAGCTCGTTG

Appendix Table S3. Thirteen genes in the mapping region

Genes	Protein family
<i>Glyma.13G053500</i>	No annotation
<i>Glyma.13G053600</i>	Malectin/receptor-like protein kinase family protein
<i>Glyma.13G053700</i>	Malectin/receptor-like protein kinase family protein
<i>Glyma.13G053800</i>	Malectin/receptor-like protein kinase family protein
<i>Glyma.13G053900</i>	Protein kinase superfamily protein
<i>Glyma.13G054000</i>	HXXXD-type acyl-transferase family protein
<i>Glyma.13G054100</i>	GAST1 protein homolog 1
<i>Glyma.13G054200</i>	Malectin/receptor-like protein kinase family protein
<i>Glyma.13G054300</i>	Malectin/receptor-like protein kinase family protein
<i>Glyma.13G054400</i>	Malectin/receptor-like protein kinase family protein
<i>Glyma.13G054500</i>	ARM repeat superfamily protein
<i>Glyma.13G054600</i>	Pectin lyase-like superfamily protein
<i>Glyma.13G054700</i>	No annotation

Appendix Table S4. Homology analysis of malectin-like RK family members on Chromosome 13 in soybean

Members of MRLK Family on Chromosome 13 in Soybean			
Gene ID	Protein Length (aa)	Identities	E-value
<i>Glyma.13G054400</i> (<i>GmLMM1</i>)	896	-	-
<i>Glyma.13G053600</i>	894	98.55%	0
<i>Glyma.13G053800</i>	702	73.80%	0
<i>Glyma.13G054300</i>	844	80.53%	0
<i>Glyma.13G053700</i>	819	79.75%	0
<i>Glyma.13G054200</i>	787	67.22%	0

Appendix Table S5. Comparison of plant height, main stem node number and other yield traits.

Genotype	Plant height; cm	Main stem node number	Single seed pod	Two seed pod	Three seed pod	Grain weight per plant; g
Williams82 n=27	120.41 ±7.16	26.85 ±1.49	27.78 ±11.01	33.56 ±15.89	28.33 ±10.94	33.11 ±12.84
<i>Gmlmm1-2</i> n=32	86.06± 7.32***	23.91± 2.51***	59.00± 21.62***	52.75± 19.06***	14.66± 7.42***	32.96± 11.90

Adult plants grown in field were used for measurements. Values given are means ± SD (***, $P < 0.001$, Student's *t*-test at).

Appendix Table S6. Chi-square test for segregation ration of F2 generation (*Gmlmm1-1* × *Gmlmm1-2*)

Cross	Generation	No. of plants/lines							
		Total	<i>Gmlmm1-1</i> gene type	<i>Gmlmm1-1</i> × <i>Gmlmm1-2</i> gene type	<i>Gmlmm1-2</i> gene type	Expected ratio	χ^2	<i>p</i>	<i>df</i>
<i>Gmlmm1-1</i> × <i>Gmlmm1-2</i>	F2	33	11	16	6	1:2:1	0.75581	0.6853	2

Appendix Table S7. Primers used in this study

Primers	sequence
GmLMM1-Nluc-F	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1-Nluc-R	aacatcgtatgggtagtcgacACGTGGCTTTGGATCCACAA
GmLMM1-CCluc-F	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1-CCluc-R	cgcgtagagatctggtcgacACGTGGCTTTGGATCCACAA
Glyma.05G198700Nluc-F	acgggggacgagctcggtaccATGGGAGGCACTTCTGCAGA
Glyma.05G198700Nluc-R	aacatcgtatgggtagtcgacGAAATTTTCTTTATGGAAGTCGACTTG
Glyma.17G226700Nluc-F	acgggggacgagctcggtaccATGCTGTCTTTTGTAAACAGAAAATATGG
Glyma.17G226700Nluc-R	aacatcgtatgggtagtcgacTAACAAGCCAGCTTCCAAGAGAT
Glyma.08G083300Nluc-F	acgggggacgagctcggtaccATGTTGTCCCTAAAGATTAGTTTGACTAT
Glyma.08G083300Nluc-R	aacatcgtatgggtagtcgacACAAGACAGTGTGTTTGAAGCTTCA
Glyma.20G008000Nluc-F	acgggggacgagctcggtaccATGGATTCTTCTGTGCCTCCTG
Glyma.20G008000Nluc-R	aacatcgtatgggtagtcgacAGGTAGTGCATCTACTACCATCCTCA
Glyma.15G051600Nluc-F	acgggggacgagctcggtaccATGGAGAGAGTGACTTCATCTTTTATGG
Glyma.15G051600Nluc-R	aacatcgtatgggtagtcgacTCTAGGACCTGATAGTTCATCTGCC
Glyma.08G180800Nluc-F	acgggggacgagctcggtaccATGGATAGAGTGACTTCGTCTTTTATG
Glyma.08G180800Nluc-R	aacatcgtatgggtagtcgacTCTAGGACCTGATAGTTCATCTGCC
Glyma.11G026400Nluc-F	acgggggacgagctcggtaccATGAGTTCCAAAGAGAGTTGCAGA
Glyma.11G026400Nluc-R	aacatcgtatgggtagtcgacGGGAGGAAAATGCTCAACATCC
Glyma.19G233900Nluc-F	acgggggacgagctcggtaccATGGAGATTCAAGTTAGAGCAGCAGC
Glyma.19G233900Nluc-R	aacatcgtatgggtagtcgacAAAATTCTCTTTATGAAAATCAAACCTTG
Glyma.12G043900Nluc-F	acgggggacgagctcggtaccATGTCTGTTACGGAGCTCAAAGAGC
Glyma.12G043900Nluc-R	aacatcgtatgggtagtcgacAGTTGTCCTCCTATGCCCTCCA
NbRXEG1-Nluc-F	acgggggacgagctcggtaccATGGGCAAAAAGGAATATCCA
NbRXEG1-Nluc-R	aacatcgtatgggtagtcgacAGCCCTTAACTTTCTCTTCAGTCTTG
NbFLS2-Nluc-F	acgggggacgagctcggtaccATGTCACAGACAGTTTTATATGCATTAGC
NbFLS2-Nluc-R	aacatcgtatgggtagtcgacAATGCAGGCATACTGGCAAATC
NbBAK1-Nluc-F	acgggggacgagctcggtaccATGGATCAATGGATATTGGGGA
NbBAK1-Nluc-R	aacatcgtatgggtagtcgacTCTTGCCCTGATAACTCATCAG
NbBAK1-FLAG-F	acgggggacgagctcggtaccATGGATCAATGGATATTGGGGA
NbBAK1-FLAG-R	atggtcttttagtcgctcgacTCTTGCCCTGATAACTCATCAG
NbFLS2-FLAG-F	acgggggacgagctcggtaccATGTCACAGACAGTTTTATATGCATTAGC
NbFLS2-FLAG-R	atggtcttttagtcgctcgacAATGCAGGCATACTGGCAAATC
NbRXEG1-FLAG-F	acgggggacgagctcggtaccATGGGCAAAAAGGAATATCCA
NbRXEG1-FLAG-R	atggtcttttagtcgctcgacAGCCCTTAACTTTCTCTTCAGTCTTG
Glyma.08G083300-FLAG-F	acgggggacgagctcggtaccATGTTGTCCCTAAAGATTAGTTTGACTAT
Glyma.08G083300-FLAG-R	atggtcttttagtcgctcgacACAAGACAGTGTGTTTGAAGCTTCA
Glyma.15G051600-FLAG-F	acgggggacgagctcggtaccATGGAGAGAGTGACTTCATCTTTTATGG
Glyma.15G051600-FLAG-R	atggtcttttagtcgctcgacTCTAGGACCTGATAGTTCATCTGCC
Glyma.08G180800-FLAG-F	acgggggacgagctcggtaccATGGATAGAGTGACTTCGTCTTTTATG
Glyma.08G180800-FLAG-R	atggtcttttagtcgctcgacTCTAGGACCTGATAGTTCATCTGCC
NbFLS2-HA-F	acgggggacgagctcggtaccATGTCACAGACAGTTTTATATGCATTAGC
NbFLS2-HA-R	aacatcgtatgggtagtcgacAATGCAGGCATACTGGCAAATC

GmLMM1-HA-F	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1-HA-R	aacatcgtatgggtagtcgacACGTGGCTTTGGATCCACAA
GmLMM1-GFP-F	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1-GFP-R	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1 ^{L407H} -GFP-F	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1 ^{L407H} -GFP-R	acgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1-FLAG-F	agaacacgggggacgagctcggtaccATGAGGCTCCTTAGCATCATCAC
GmLMM1-FLAG-R	tggtcttttagtcgacACGTGGCTTTGGATCCACAA
BIK1-HIS-F	taagaaggagatataccatggTTCTTGCTTCAGTTCTCGAGTCA
BIK1-HIS-R	gtggtggtggtgctcgagCACAAGGTGCCTGCCAAAA
GmLMM1KD-HIS-F	taagaaggagatataccatggCCGCGCTGGACTGCATT
GmLMM1KD-HIS-R	gtggtggtggtgctcgagAACGACGTCGTTCATCGACG
CRISPR 9 -F	ATTGCGAGGCACTGCTGCCAAAA
CRISPR 9 -R	AACCTTTGGCAGCAGTGCCTCGC
CRISPR 1 -F	ATTGATCTTTCAAGCAACACGGA
CRISPR 1 -R	AACCTCCGTGTTGCTTGAAAGATC
CRISPR 2 -F	ATTGGAACCGCAGCAGCAAAAG
CRISPR 2 -R	AACCTTTTGCTGCTGCGGTTTCC
CRISPR-R	GATGAAGTGGACGGAAGGAAGGAG
BlpR-F	ATGACAGCGACCACGCTCTTGAAG
BlpR-R	CTGCACCATCGTCAACCACTACATC
gDNA-GmLMM1-F	GAGGGAAAAGCAGTTATTG
gDNA-GmLMM1-R	GCCAATTACGTTGCTGTTG
gDNA-Glyma.13G053600-F	TTTAAGGCAATTTAGGTGGG
gDNA-Glyma.13G053600-R	TTCTGGAAGTGTGAGGCT
gDNA-Glyma.13G053800-F	GATTCCACCTTGATCTTCCTAA
gDNA-Glyma.13G053800-R	AAGTGTAACATGACTCCCCATA
GmELF1 β -F	GTTGAAAAGCCAGGGGACA
GmELF1 β -R	TCTTACCCCTTGAGCGTGG
GmPR1-F	ACCGGTAACCTAAGTGGTACAAATG
GmPR1-R	CCACATCCAAGACGCACAGAGT
GmPR2-F	GTCTCCTTCGGTGGTAGTG
GmPR2-R	ACCCTCCTCCTGCTTCTC
PsTEF1-F	TGATCGTGCTGAACCAACC
PsTEF1-R	CGAGCGACGGTCCATCTT
AvrB-kpnI-F	CGGGGGACGAGCTCGGTACCATGGGCTGCGTCTCGTCAAA
AvrB-SalI-R	TGGTCTTTGTAGTCGTCGACTTAAAAGCAATCAGAATCTA
AvrRpt2-kpnI-F	CGGGGGACGAGCTCGGTACCATGAAAATTGCTCCAGTTGC
AvrRpt2-SalI-R	TGGTCTTTGTAGTCGTCGACTTAGCGGTAGAGCATTGCGT
